

Technical University of Denmark



Does reactor staging influence microbial structure and functions in biofilm systems? The case of pre-denitrifying MBBRs

Polesel, Fabio; Torresi, Elena; Jensen, Marlene Mark; Fowler, Jane; Escola Casas, Monica; Smets, Barth F.; Christensson, Magnus; Bester, Kai; Plósz, Benedek G.

Publication date:
2016

Document Version
Peer reviewed version

[Link back to DTU Orbit](#)

Citation (APA):
Polesel, F., Torresi, E., Jensen, M. M., Fowler, J., Escola Casas, M., Smets, B. F., ... Plósz, B. G. (2016). Does reactor staging influence microbial structure and functions in biofilm systems? The case of pre-denitrifying MBBRs. Abstract from International Conference on Emerging Contaminants (EmCon2016) and Micropollutants (WiOW2016) in the Environment, Sydney, Australia.

DTU Library
Technical Information Center of Denmark

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Please tick the relevant category:

Platform X

Poster

Either

Does reactor staging influence microbial structure and functions in biofilm systems? The case of pre-denitrifying MBBRs

Fabio Polese¹, Elena Torresi¹, Marlene M. Jensen¹, Jane Fowler¹, Monica Escolá Casas², Barth F. Smets¹, Magnus Christensson³, Kai Bester², Benedek Gy. Plósz¹

¹*Department of Environmental Engineering, Technical University of Denmark, Kgs. Lyngby, Denmark, fabp@env.dtu.dk, elto@env.dtu.dk, mmaj@env.dtu.dk, jfow@env.dtu.dk, beep@env.dtu.dk, bfsm@env.dtu.dk*

²*Department of Environmental Science, Aarhus University, Roskilde, Denmark, kb@envs.au.dk*

³*Veolia Water Technologies AB, AnoxKaldnes, Lund, Sweden, magnus.christensson@anoxkaldnes.com*

To date, a number of treatment technologies and configurations have been tested to improve the elimination of conventional and trace (e.g., pharmaceutical residues) pollutants via biological wastewater treatment. Bioreactor staging and the moving bed biofilm reactor (MBBR) technology have emerged as promising bioengineered solutions (Plósz et al., 2010) for this purpose. In this study, we combined the two solutions and investigated microbial functions (heterotrophic denitrification, pharmaceutical removal) and structure of the microbial community in staged MBBRs for pre-denitrification. A three-stage MBBR system (S1+S2+S3), fed with pre-clarified wastewater, was operated at laboratory-scale with (i) controlled biomass exposure to organic substrate (COD); and (ii) enhanced the physical retention of biomass, thus inducing adaptation to different substrate exposure conditions. During long-term operation (~500 days) of the three-stage MBBR under continuous-flow conditions, biofilm samples were collected to assess the temporal evolution of the microbial structure in terms of functional gene abundance and biodiversity. A set of batch experiments (day 471) was performed to assess denitrification and pharmaceutical removal in each MBBR, following prolonged biofilm exposure to specific COD availability.

Results from batch experiments showed declining denitrification potential and pharmaceutical biotransformation rate constants (k_{bio} , L gTSS⁻¹ d⁻¹) from MBBR S1 (exposed to highest COD availability) to S3 (exposed to lowest availability). These findings indicate that the exposure to tiered substrate availability influenced the capacity of utilizing a different range of carbon sources in each MBBR, thus impacting denitrification and pharmaceutical biotransformation. Preliminary analysis on the microbial community based on qPCR (quantitative polymerase chain reaction) showed differences in the abundance of genes (*nirS*, *nirK*, *nosZ*) encoding for denitrifying enzymes in the three staged MBBRs. Further microbial characterization through 16sRNA sequencing (Illumina) is currently under investigation to determine whether differences in microbial functions should be associated to differences in the microbial diversity in the three MBBRs.

Keywords: Moving bed biofilm reactors; reactor staging; pharmaceuticals; denitrification; qPCR; DNA sequencing

References

Plósz, B.G., et al. (2010) The BIOZO process - a biofilm system combined with ozonation: occurrence of xenobiotic organic micro-pollutants in and removal of polycyclic aromatic hydrocarbons and nitrogen from land-fill leachate. *Water Sci. Technol.* 61(12), 3188–3197.